GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: October 22, 2003, 14:52:59 ; Search time 1133 Seconds
(without alignments)
1.687 Million cell updates/sec

Title: CER06C7
Perfect score: 30911
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 30911 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1 summaries

Database : 24-sep-2003-z71266:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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ALIGNMENTS

RESULT 1
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DEFINITION Caenorhabditis elegans cosmid R06C7, complete sequence.
ACCESSION Z71266
VERSION Z71266.1 GI:1279324
KEYWORDS HTG; Adenylosuccinate lyase; Myosin heavy chain; Rat TOAD-64 protein like; Serine/threonine-protein kinase; Zinc finger protein.
SOURCE Caenorhabditis elegans
ORGANISM Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE 1
AUTHORS none.
TITLE Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium
JOURNAL Science 282 (5396), 2012-2018 (1998)
MEDLINE 99069613
PUBMED 9851916
REMARK The C.elegans Sequencing Consortium.
REFERENCE 2 (bases 1 to 30911)
AUTHORS Gardner,A.E.
TITLE Direct Submission
JOURNAL Submitted (19-APR-1996) Nematode Sequencing Project, Sanger Institute, Hinxton, Cambridge CB10 1SA, England and Department of Genetics, Washington University, St. Louis, MO 63110, USA. E-mail: jes@sanger.ac.uk or rw@nematode.wustl.edu

COMMENT Coding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Washington), and other available information.
Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.
IMPORTANT: This sequence is not the entire insert of clone R06C7. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.
The true left end of clone R06C7 is at 1 in this sequence. The true right end of clone R06C7 is at 8718 in sequence Z71261.
The true left end of clone F21C3 is at 30808 in this sequence. The start of this sequence (1..106) overlaps with the end of sequence Z98261.
The end of this sequence (30808..30911) overlaps with the start of sequence Z71261.
For a graphical representation of this sequence and its analysis see:- http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?name=R06C7
IMPORTANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

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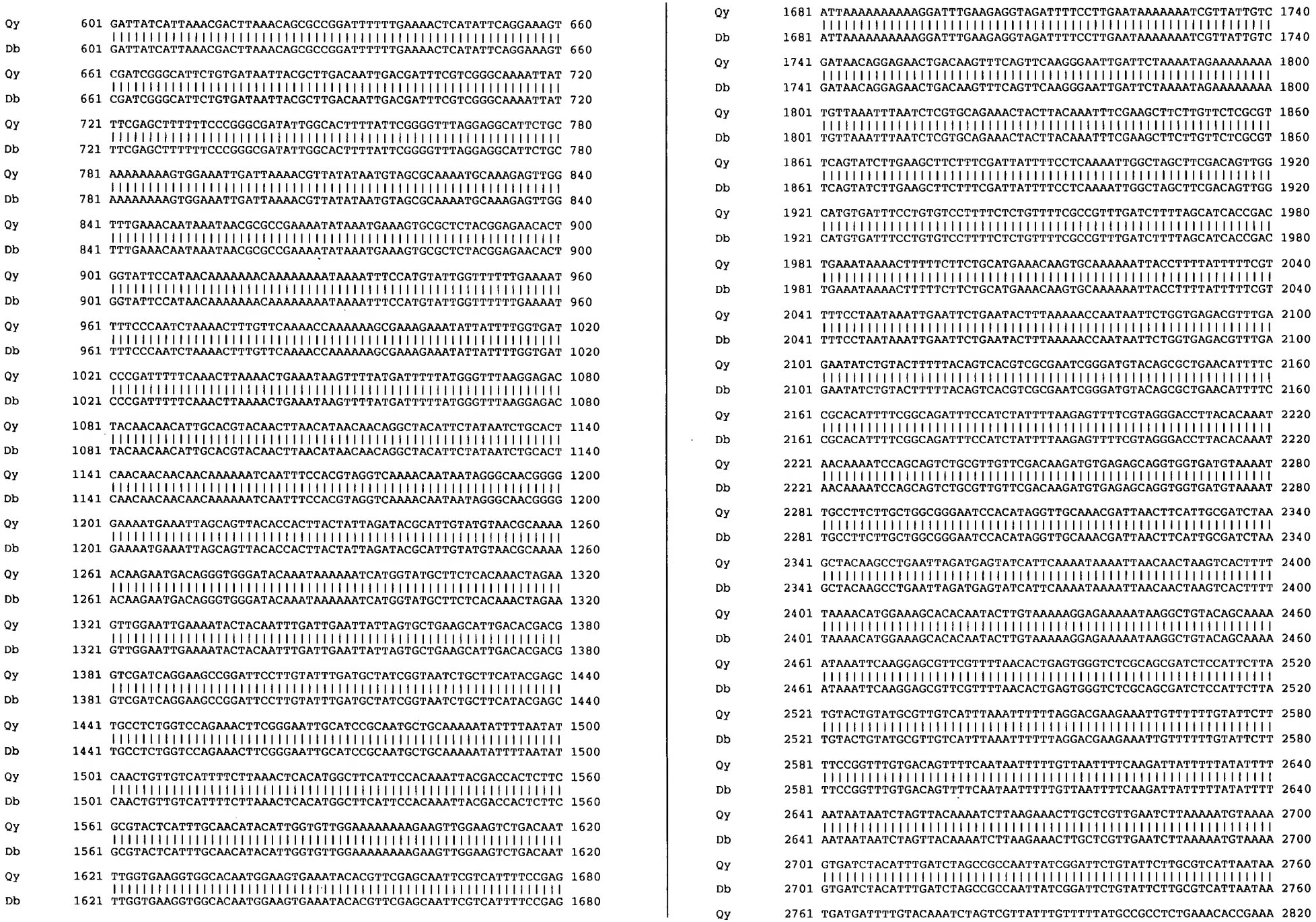
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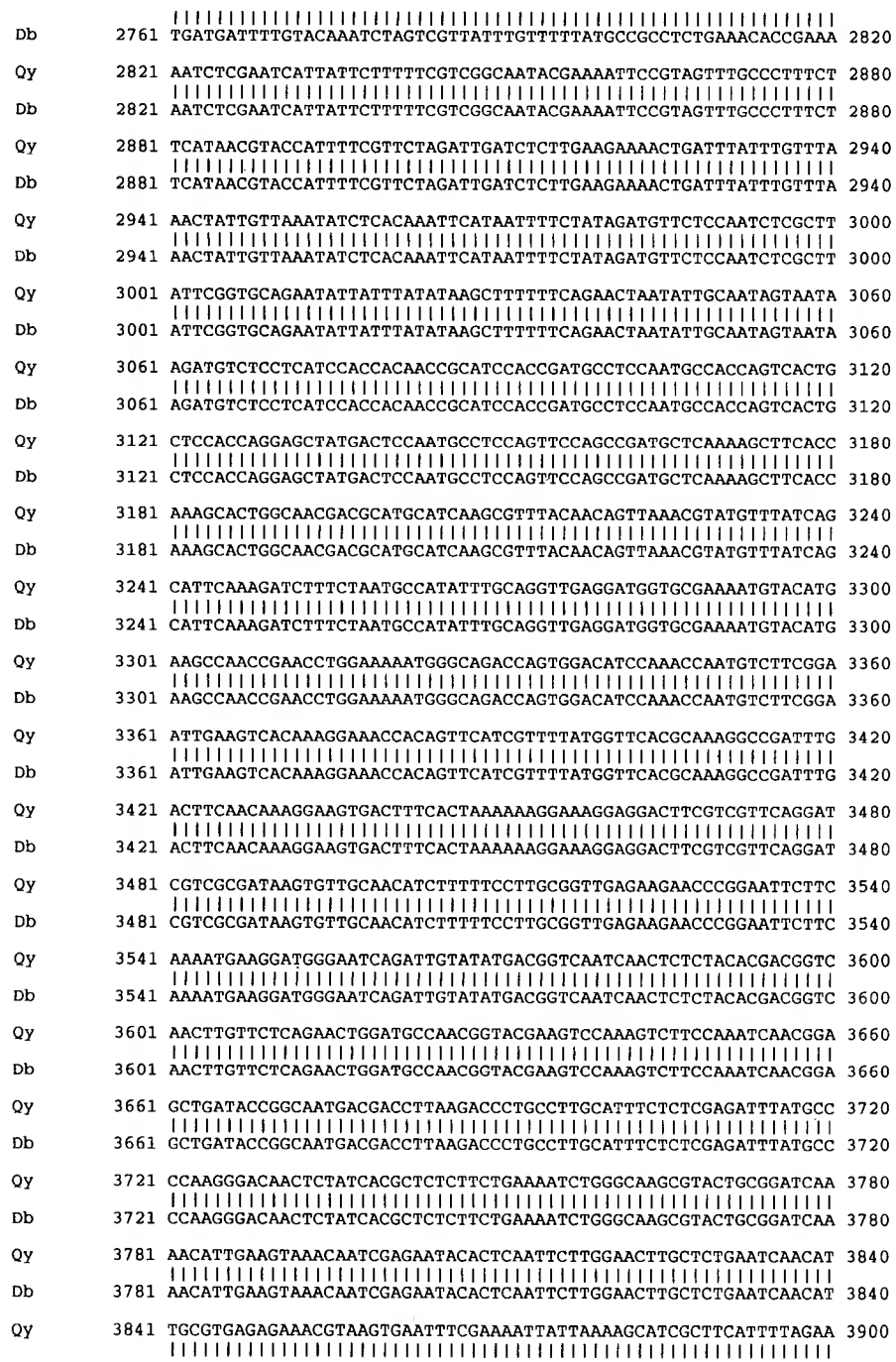
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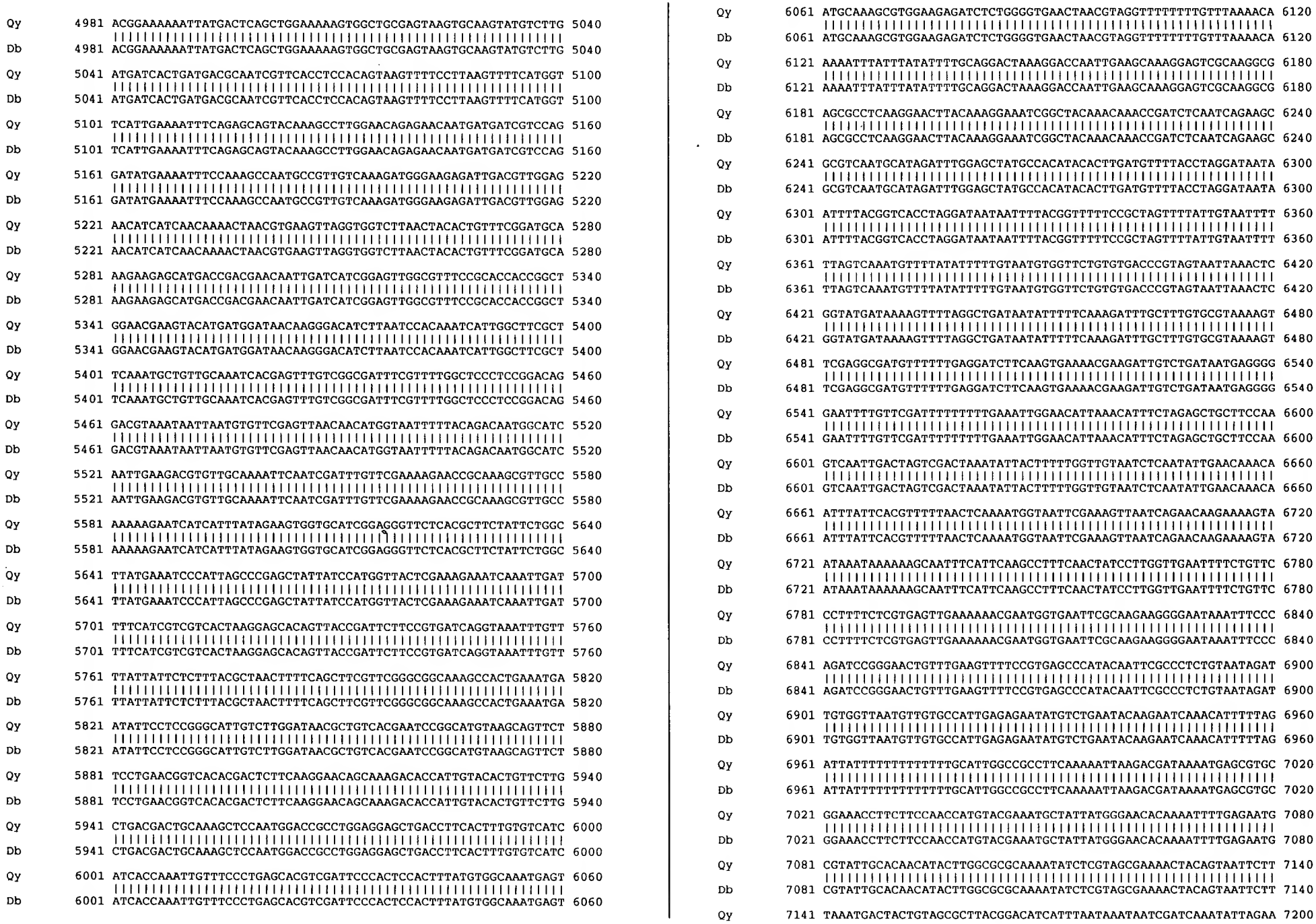
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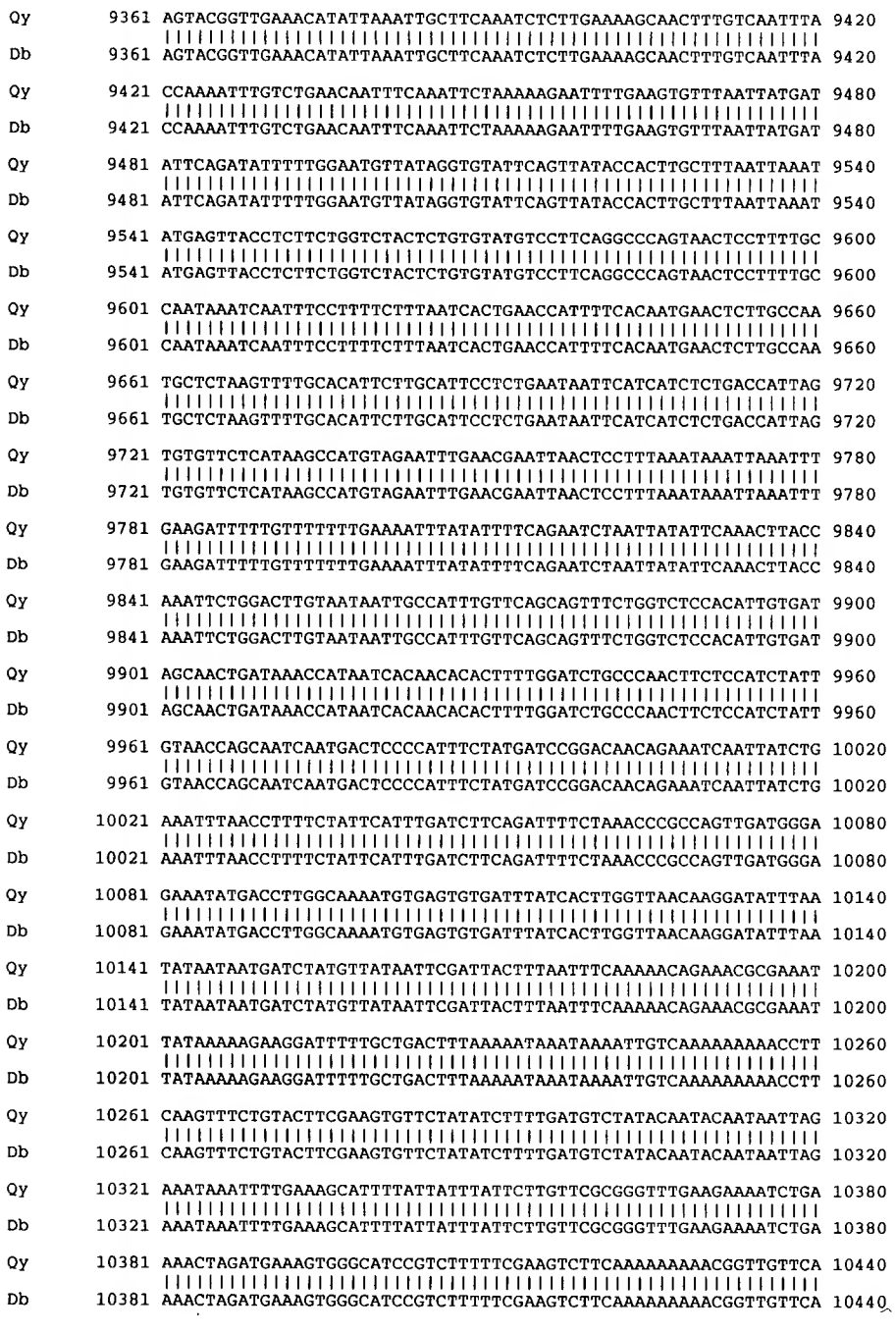
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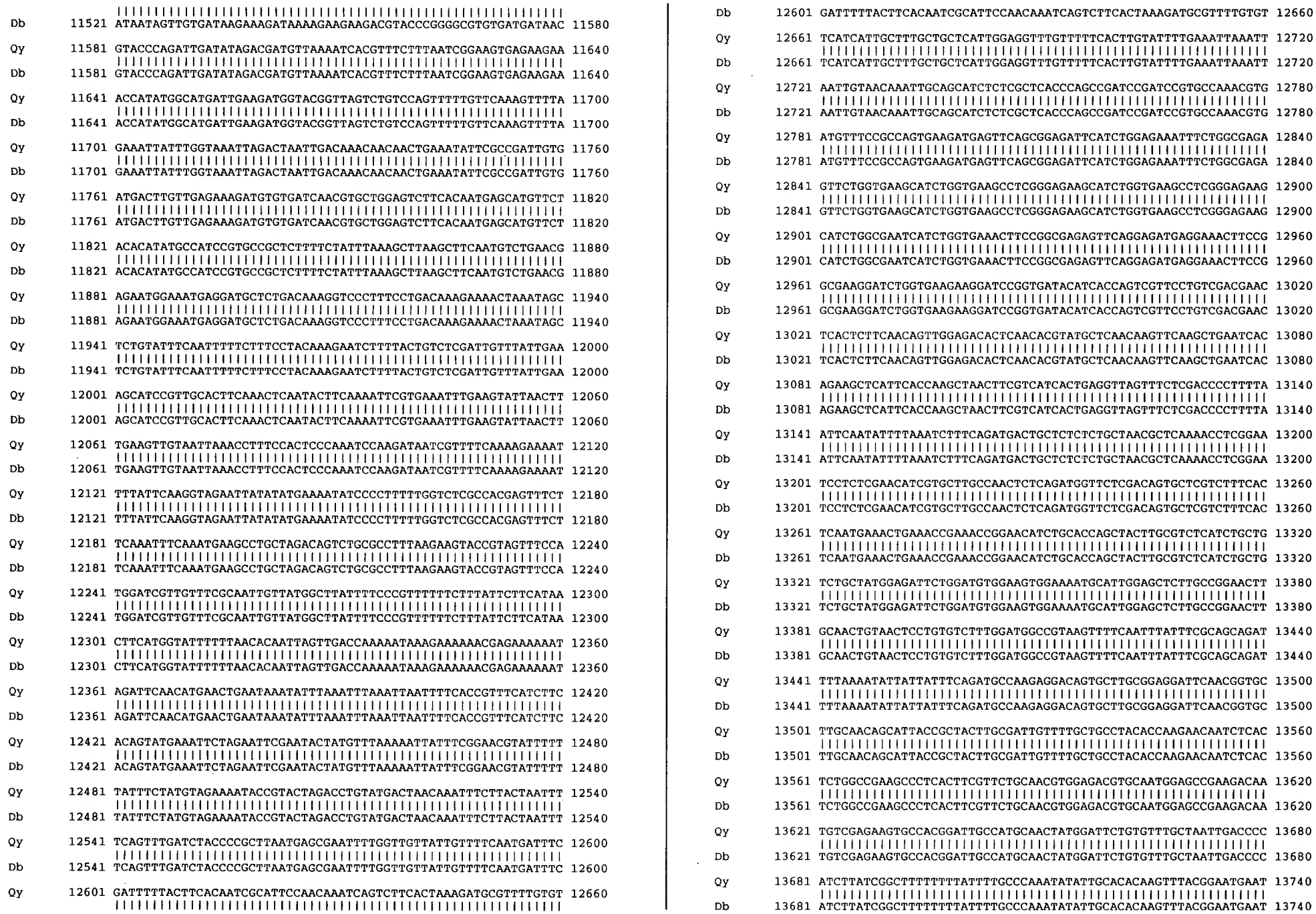
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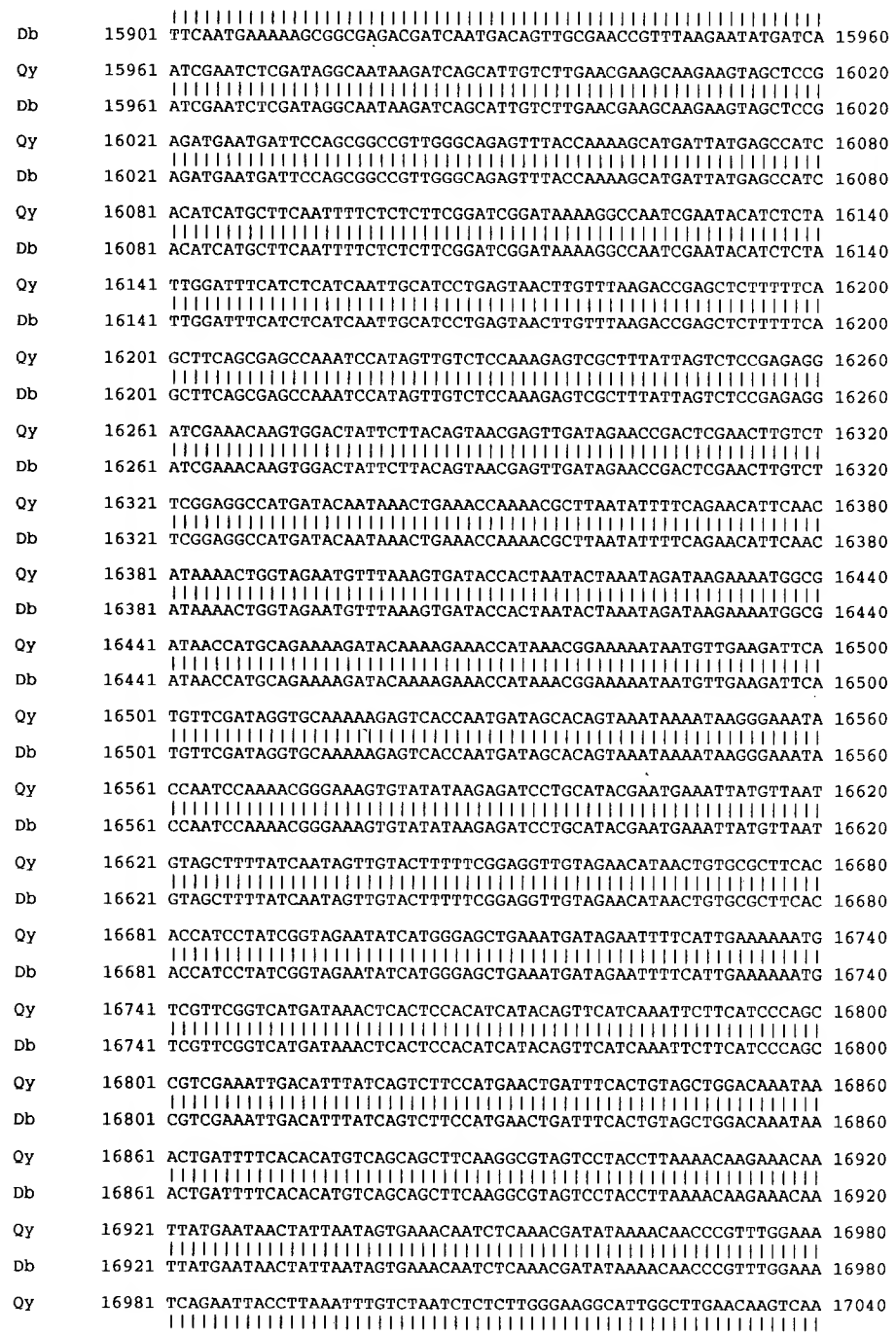
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Qy      20821 GCTTCTGCAAGAACATCAAAGAGTGGAGCTGGATTGGATTTGATGGCGGAAAATAAGTGT 20880

Db      20821 GCTTCTGCAAGAACATCAAAGAGTGGAGCTGGATTGGATTTGATGGCGGAAAATAAGTGT 20880

Qy      20881 TTGGAGGCACATGCTATGTTTTCCGACACTGTACATCTTGCTAGCGAAAAGACAATGGTC 20940

Db      20881 TTGGAGGCACATGCTATGTTTTCCGACACTGTACATCTTGCTAGCGAAAAGACAATGGTC 20940

Qy      20941 CTTGGCGATGATTCTGTCTTCGTTCCAGAAAGATCTTTAGCTACTACGCAGATAGTTACT 21000

Db      20941 CTTGGCGATGATTCTGTCTTCGTTCCAGAAAGATCTTTAGCTACTACGCAGATAGTTACT 21000

Qy      21001 GACTTTTCCGTGCTCTGTGATCCTGATCCGACAATGACCATTACACAGGAGCGTCCGAAA 21060

Db      21001 GACTTTTCCGTGCTCTGTGATCCTGATCCGACAATGACCATTACACAGGAGCGTCCGAAA 21060

Qy      21061 AAAGTGTCGAATGGGTTGAATGTTGTTTACGATGAGGCAGCCGAACCGGAAGAATCTCAG 21120

Db      21061 AAAGTGTCGAATGGGTTGAATGTTGTTTACGATGAGGCAGCCGAACCGGAAGAATCTCAG 21120

Qy      21121 AAAGTTGAGGAATCTGAAGTACAACCCGAAATTGTCCTAGTTTCTCCAGTGACGCAAACC 21180

Db      21121 AAAGTTGAGGAATCTGAAGTACAACCCGAAATTGTCCTAGTTTCTCCAGTGACGCAAACC 21180

Qy      21181 TCACCAGCTACAATGTTTAATGATAGTGGGTTTATCGAAAAATATAACAACTTATGTTTT 21240

Db      21181 TCACCAGCTACAATGTTTAATGATAGTGGGTTTATCGAAAAATATAACAACTTATGTTTT 21240

Qy      21241 AATTTTTAGTTTATGACGATGAAATCGAGTTTGGCTTTTTCAAACCGTCTCGTGGTAATT 21300

Db      21241 AATTTTTAGTTTATGACGATGAAATCGAGTTTGGCTTTTTCAAACCGTCTCGTGGTAATT 21300

Qy      21301 TCGTCACATCGACCCCCGCACAAGGAGTTCATTTGGTCAACATTGATGAATATTTCGGAA 21360

Db      21301 TCGTCACATCGACCCCCGCACAAGGAGTTCATTTGGTCAACATTGATGAATATTTCGGAA 21360

Qy      21361 ATAAAGAGGAGGAAAGCACTCACGAACAGGAAGCTCCAGTATTTGTTGCTCCAACCAGCA 21420

Db      21361 ATAAAGAGGAGGAAAGCACTCACGAACAGGAAGCTCCAGTATTTGTTGCTCCAACCAGCA 21420

Qy      21421 GTACTTTCAGTAAATTAGTAAGTGCCAGACAAATTTTCGACATACTATTCAAACTTTTTC 21480

Db      21421 GTACTTTCAGTAAATTAGTAAGTGCCAGACAAATTTTCGACATACTATTCAAACTTTTTC 21480

Qy      21481 AGACACGTCGAAAGTCACTAGCAGCAAATCAAGCCGTTCAGCCCTCAGTCACAGAGTCAT 21540

Db      21481 AGACACGTCGAAAGTCACTAGCAGCAAATCAAGCCGTTCAGCCCTCAGTCACAGAGTCAT 21540

Qy      21541 CAAAGCCTGAACGATCAGATCCTAAAGATTCATCTATCGATTGTTTGACAGCTAATCTAG 21600

Db      21541 CAAAGCCTGAACGATCAGATCCTAAAGATTCATCTATCGATTGTTTGACAGCTAATCTAG 21600

Qy      21601 GAAGACGTCTTTCAATTGGTGCTGATGAAATTCCAAATCTCACTGAAAACAACGAATCTG 21660

Db      21601 GAAGACGTCTTTCAATTGGTGCTGATGAAATTCCAAATCTCACTGAAAACAACGAATCTG 21660

Qy      21661 AAATCACTGGTTGCAAGATTCGTCGGCGCAGTGAAATTATCAAGCAAGGAGACATCAATC 21720

Db      21661 AAATCACTGGTTGCAAGATTCGTCGGCGCAGTGAAATTATCAAGCAAGGAGACATCAATC 21720

Qy      21721 CATGGGACGAAACTCTTCGAAAAAAATTGATGTGTCTTGTGCGTCCTCCCCAGAATATGC 21780

Db      21721 CATGGGACGAAACTCTTCGAAAAAAATTGATGTGTCTTGTGCGTCCTCCCCAGAATATGC 21780

Qy      21781 ACGAGTTCCAAGAACGAGCACCGAAGATTCAAGCTCTGAGAGACTGCGAGGTTAGCGGAG 21840

Db      21781 ACGAGTTCCAAGAACGAGCACCGAAGATTCAAGCTCTGAGAGACTGCGAGGTTAGCGGAG 21840

Qy      21841 AAAAGCTCCACATTCAAACTCTTATTGGTCAAGGTGGATACGCTAAAGTATACCGGGCTG 21900

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Qy      21901 TAACCGATGATCAAAGGACAGTAGCTGTGAAGTACGAGGTGCCATCATGTTCGTGGGAAG 21960

Db      21901 TAACCGATGATCAAAGGACAGTAGCTGTGAAGTACGAGGTGCCATCATGTTCGTGGGAAG 21960

Qy      21961 TGTACATTTGCGACCAAATGCGGAATCGCCTGAAAGATCGAGGTTTGGAGCTGATGGCCA 22020

Db      21961 TGTACATTTGCGACCAAATGCGGAATCGCCTGAAAGATCGAGGTTTGGAGCTGATGGCCA 22020

Qy      22021 AATGTTGCATTATGGAAGTGATGGATGCTTATGTTTATTCAACTGCTTCGCTTCTTGTTA 22080

Db      22021 AATGTTGCATTATGGAAGTGATGGATGCTTATGTTTATTCAACTGCTTCGCTTCTTGTTA 22080

Qy      22081 ATCAGTACCACGAATATGGAACGCTGCTTGAATATGCGAATAACATGAAGGATCCGAATT 22140

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Db      22141 GGCACATAACCTGCTTCTTGATTACCCAAATGGCCCGAGTTGTGAAGGAAGTCCATGCCT 22200

Qy      22201 CTAAAATTATTCATGGAGATATCAAACCGGATAATTTTATGATCACCAGAAAGTATGGGA 22260

Db      22201 CTAAAATTATTCATGGAGATATCAAACCGGATAATTTTATGATCACCAGAAAGTATGGGA 22260

Qy      22261 AAACATTTGTTAATTTTAGACGTTATCTTTTTTCAGGATCGATGATAAATGGGGCAAAGA 22320

Db      22261 AAACATTTGTTAATTTTAGACGTTATCTTTTTTCAGGATCGATGATAAATGGGGCAAAGA 22320

Qy      22321 TGCTCTGATGAGTAACGACAGCTTTGTCATCAAGATTATCGACTGGGGACGTGCCATTGA 22380

Db      22321 TGCTCTGATGAGTAACGACAGCTTTGTCATCAAGATTATCGACTGGGGACGTGCCATTGA 22380

Qy      22381 CATGATGCCACTGAAGAACCAGCGTTTCAAGGGAAGAGCAGGAACAGAAGCGTTTGATTG 22440

Db      22381 CATGATGCCACTGAAGAACCAGCGTTTCAAGGGAAGAGCAGGAACAGAAGCGTTTGATTG 22440

Qy      22441 CCCGGAAATGGTTGACGGTCGTTCTTGGACTTACCAAGCCGATTACTTCGGATTCGCCGC 22500

Db      22441 CCCGGAAATGGTTGACGGTCGTTCTTGGACTTACCAAGCCGATTACTTCGGATTCGCCGC 22500
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Qy      22501 AACAATGGCTGTCGTTGTTGCAGGAAAGTATGCACAGTTGACTGGAGCTAGCGTTGGAGA 22560
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Db      22501 AACAATGGCTGTCGTTGTTGCAGGAAAGTATGCACAGTTGACTGGAGCTAGCGTTGGAGA 22560

Qy      22561 CTATTCGTTAAATGTCGACATCAAGAGGCGCAACATTCTTCGCGATGCTTGCTACGATGT 22620
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Db      22561 CTATTCGTTAAATGTCGACATCAAGAGGCGCAACATTCTTCGCGATGCTTGCTACGATGT 22620

Qy      22621 CATTAACAGATTCCTCAACATCCCTTCGTGTGATTCACTTCCGGACTGGAATATCCTGAT 22680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      22621 CATTAACAGATTCCTCAACATCCCTTCGTGTGATTCACTTCCGGACTGGAATATCCTGAT 22680

Qy      22681 CAAGTCTTTCTCGGAAATCTGGAATGAAAAGTTTGAAGCATCGGGATGGCGACAGGCGGT 22740
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Db      22681 CAAGTCTTTCTCGGAAATCTGGAATGAAAAGTTTGAAGCATCGGGATGGCGACAGGCGGT 22740

Qy      22741 TTCCAAGTTCAATGAGGCCTGTGATCTTGCCGCCAACCAAAAGTAGCCCAACACAATGAA 22800
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Db      22741 TTCCAAGTTCAATGAGGCCTGTGATCTTGCCGCCAACCAAAAGTAGCCCAACACAATGAA 22800

Qy      22801 TTTGTATTTCGTGCTCTTATTGCTCTCTTTTATTGTCTTTTGTATTGATATCATGTGAAT 22860
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Db      22801 TTTGTATTTCGTGCTCTTATTGCTCTCTTTTATTGTCTTTTGTATTGATATCATGTGAAT 22860

Qy      22861 AAACTCGTTCGGAGCTTTAATAATTGTGCATCTAATTTATTTCTGGTAAAACAAATTGAA 22920
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Db      22861 AAACTCGTTCGGAGCTTTAATAATTGTGCATCTAATTTATTTCTGGTAAAACAAATTGAA 22920

Qy      22921 TTAAACGAAGTTTTCAGTTTTTGAAAGCTTTCCAAATTTGAACGTGATATTCGAGATTGG 22980
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      22921 TTAAACGAAGTTTTCAGTTTTTGAAAGCTTTCCAAATTTGAACGTGATATTCGAGATTGG 22980

Qy      22981 GCGCGGCGAGACCCATCACGGTAGAAATTTGATGCGCCTTTAAAGGGAAGTATTGCAATA 23040
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Db      22981 GCGCGGCGAGACCCATCACGGTAGAAATTTGATGCGCCTTTAAAGGGAAGTATTGCAATA 23040

Qy      23041 GATCACAGTTAGATCTAAATAGTTGCACATTCGTTTTGTTTCATCAACTGTTTTCTTCGC 23100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      23041 GATCACAGTTAGATCTAAATAGTTGCACATTCGTTTTGTTTCATCAACTGTTTTCTTCGC 23100

Qy      23101 GTTTTGCATAAAATGTGATATTTAAAAAAGAATTTAGAAAAAATTACAATTAAAATATTT 23160
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Db      23101 GTTTTGCATAAAATGTGATATTTAAAAAAGAATTTAGAAAAAATTACAATTAAAATATTT 23160

Qy      23161 TCCAGCCATCCTCTTGTAAAAATGGAAGAATCAGATCAGACTGTGGTGAGCGCTAGTGTT 23220
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Db      23161 TCCAGCCATCCTCTTGTAAAAATGGAAGAATCAGATCAGACTGTGGTGAGCGCTAGTGTT 23220

Qy      23221 TAATCAACTTATTTTGCAAAAAGTTTCAGCTTTTACCAAATGTCGAAAATGAAATTGGCA 23280
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Db      23221 TAATCAACTTATTTTGCAAAAAGTTTCAGCTTTTACCAAATGTCGAAAATGAAATTGGCA 23280

Qy      23281 GTTTTTATCATGACATGCCTGATGAAAAATTGCTTCGTCATATCAAAGCAATTTTCGACG 23340
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Db      23281 GTTTTTATCATGACATGCCTGATGAAAAATTGCTTCGTCATATCAAAGCAATTTTCGACG 23340

Qy      23341 AAGCTTCACTTCGACCATCTTTGGTATTTAATCTTCATTGAAACCTCAACATAAAGTTAG 23400
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Db      23341 AAGCTTCACTTCGACCATCTTTGGTATTTAATCTTCATTGAAACCTCAACATAAAGTTAG 23400

Qy      23401 AGTTGTAGACTAAAAACGTGCCATCCACATCTTCACAAGTCACAGAGGAATTGAATAAAG 23460
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Db      23401 AGTTGTAGACTAAAAACGTGCCATCCACATCTTCACAAGTCACAGAGGAATTGAATAAAG 23460

Qy      23461 TTGAAATCAGAGATCCAAAGCATGAAATGCAAGATGAGGTTGAAATATAAATTTGGTAAA 23520
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Db      23461 TTGAAATCAGAGATCCAAAGCATGAAATGCAAGATGAGGTTGAAATATAAATTTGGTAAA 23520

Qy      23521 AATGCTGTATAATTTTCGAATTCCAGCAATATCTTTCAATATTCGAAAATCCGTCCGGAG 23580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      23521 AATGCTGTATAATTTTCGAATTCCAGCAATATCTTTCAATATTCGAAAATCCGTCCGGAG 23580

Qy      23581 TTCAGTACAACCAAGCTGATGGCTCATTTTCGTGGAATAATCGCTTCCATAGTGTAAAAA 23640
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Db      23581 TTCAGTACAACCAAGCTGATGGCTCATTTTCGTGGAATAATCGCTTCCATAGTGTAAAAA 23640

Qy      23641 CCAACTGTAATTCATTTTCTAATGAACATTTTCAGGACAACAGCGTCCAATACATAAACG 23700
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      23641 CCAACTGTAATTCATTTTCTAATGAACATTTTCAGGACAACAGCGTCCAATACATAAACG 23700

Qy      23701 TGTTGAACAACTATGGTTGTGAAGGTGCTGATACACTATTAAATCAGTCAGACAGTAGCG 23760
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Db      23701 TGTTGAACAACTATGGTTGTGAAGGTGCTGATACACTATTAAATCAGTCAGACAGTAGCG 23760

Qy      23761 ATGAAACCGATGAAAGTATCGAAGAAAGACGGACCCCACGAGGAAACCGGCAGTCGCGTA 23820
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Db      23761 ATGAAACCGATGAAAGTATCGAAGAAAGACGGACCCCACGAGGAAACCGGCAGTCGCGTA 23820

Qy      23821 GTAATTTGACATCGAAACCCTCTGCCAAATATTGGACAAAAAGAGGAGGAGATCCAATTG 23880
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Db      23821 GTAATTTGACATCGAAACCCTCTGCCAAATATTGGACAAAAAGAGGAGGAGATCCAATTG 23880

Qy      23881 TTAATTGCTCGGTTAGTTCATTTTAGTTCTATATCTCATTCTCTGTAAATGAACAAAAAC 23940
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Db      23881 TTAATTGCTCGGTTAGTTCATTTTAGTTCTATATCTCATTCTCTGTAAATGAACAAAAAC 23940

Qy      23941 CTTCACTATTATCACTATTATACCATATCACTATTATAGATTTATTTATTACAACTTAAA 24000
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      23941 CTTCACTATTATCACTATTATACCATATCACTATTATAGATTTATTTATTACAACTTAAA 24000

Qy      24001 AGTGTGTACCAACCATCAAATTTCTCAAAATCTAAAGCATAACATTCTGAACATGATTTT 24060
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      24001 AGTGTGTACCAACCATCAAATTTCTCAAAATCTAAAGCATAACATTCTGAACATGATTTT 24060

Qy      24061 ATTCTTCAATTTCAGTGCTCAATATGTGGATCCAAATTTTCAACCATTCGCTGTCTTCTT 24120
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Db      24061 ATTCTTCAATTTCAGTGCTCAATATGTGGATCCAAATTTTCAACCATTCGCTGTCTTCTT 24120

Qy      24121 GATCATCGTCATCAAGAACATTCACTGAAAGATATGATGATGTGTGGTCTCTGTGGAAAA 24180
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Db      24121 GATCATCGTCATCAAGAACATTCACTGAAAGATATGATGATGTGTGGTCTCTGTGGAAAA 24180

Qy      24181 GAGTTTTCGAAGCGAACACATATCTATTTGCATCTAAGTCAAGAATACAAAGTATATCAT 24240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      24181 GAGTTTTCGAAGCGAACACATATCTATTTGCATCTAAGTCAAGAATACAAAGTATATCAT 24240

Qy      24241 TGTGACGGTTGCAATACATCGTTTGCCAGCAAATGGCACTTGGAAAAGCATCGATGTAAG 24300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      24241 TGTGACGGTTGCAATACATCGTTTGCCAGCAAATGGCACTTGGAAAAGCATCGATGTAAG 24300

Qy      24301 GAAAATGAAACAATCGACGATAAAAAACGAAGAAGAACGGGACGTGTAAATGCGGAAGAA 24360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      24301 GAAAATGAAACAATCGACGATAAAAAACGAAGAAGAACGGGACGTGTAAATGCGGAAGAA 24360

Qy      24361 ATAAAAGTAATAAAAGAAGAGATTCAAGATGAAGAATTTGGTGGCGTTGTTTTGTCTAAT 24420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      24361 ATAAAAGTAATAAAAGAAGAGATTCAAGATGAAGAATTTGGTGGCGTTGTTTTGTCTAAT 24420

Qy      24421 GAGAATCATGAAAAATCAAAAGAAGACCGTTTCCAATTCGCTTGTGTATTATGTGGAAAG 24480
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Db      24421 GAGAATCATGAAAAATCAAAAGAAGACCGTTTCCAATTCGCTTGTGTATTATGTGGAAAG 24480

Qy      24481 AAATATCAACACTATCATTGGTTGCTCAAACATAGAACCAAATGCTTGGAAACAACGGAC 24540
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Db      24541 GAAATTCAGGTGGAGAATGTTTAGTGAAACGTTTTTGCGAGAACTTCACTAATTGAAAAT 24600

Qy      24601 ATAAACTAATTTAACAGATTATTTTTTCTTGTTTTACAAAAAAAAAATAAATTTCAGTCA 24660
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Db      24601 ATAAACTAATTTAACAGATTATTTTTTCTTGTTTTACAAAAAAAAAATAAATTTCAGTCA 24660

Qy      24661 GAGATGGGACATAAACATTGTTTTGCAGGAATTCAAGTGCAATGTTTGCTACCGAAGATA 24720
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Db      24661 GAGATGGGACATAAACATTGTTTTGCAGGAATTCAAGTGCAATGTTTGCTACCGAAGATA 24720
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Db      26461 GGAGTTCCTGGAAAAAACCACAGCGCGAAACCGTACTACTTGAGTGAAGTATCCTGCCAG 26520
Qy      26521 ATCCTGGTGTCTTATCATCATTTGTGCAGAGTAAATAGAAAAGAAGAAAGAAAGAAAGAG 26580
Db      26521 ATCCTGGTGTCTTATCATCATTTGTGCAGAGTAAATAGAAAAGAAGAAAGAAAGAAAGAG 26580
Qy      26581 ATTGTATTTACATAAGAGAGTCTTAATTACAACTTTATTCTTGAAAAAGAAGAGTTGATG 26640
Db      26581 ATTGTATTTACATAAGAGAGTCTTAATTACAACTTTATTCTTGAAAAAGAAGAGTTGATG 26640
Qy      26641 ATGATGATGACAGACACACCGTTTGCGTTTTTTGAATTGATTTGATTTTCTAGAGCCTGG 26700
Db      26641 ATGATGATGACAGACACACCGTTTGCGTTTTTTGAATTGATTTGATTTTCTAGAGCCTGG 26700
Qy      26701 GGCTTTTGGAAGGCAGTTTACTGATTGATAATGTGGAGGGTCGATCGCTAGAATCGAAAG 26760
Db      26701 GGCTTTTGGAAGGCAGTTTACTGATTGATAATGTGGAGGGTCGATCGCTAGAATCGAAAG 26760
Qy      26761 AATTATGATGTCAACGAGACTTTCAGATTATATCAATTTCAGACGTGTGGAGCGTCGGGA 26820
Db      26761 AATTATGATGTCAACGAGACTTTCAGATTATATCAATTTCAGACGTGTGGAGCGTCGGGA 26820
Qy      26821 GAAATCAACAGAATTTAAAGATCAACGGAGACTCGGCGCGCGAATCGTTCAAACAGAGAG 26880
Db      26821 GAAATCAACAGAATTTAAAGATCAACGGAGACTCGGCGCGCGAATCGTTCAAACAGAGAG 26880
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Qy      26881 TGAGAGAATATGATTGAGACTGAAACTTTAACAATTAGGAAAAAGGAAACTGAGAAAAAC 26940
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Db      26881 TGAGAGAATATGATTGAGACTGAAACTTTAACAATTAGGAAAAAGGAAACTGAGAAAAAC 26940

Qy      26941 TTGATTATAAACAAGATATGTGGGGGAAAATACAAAACTATGAGAAATTATTTGTGTGTG 27000
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      26941 TTGATTATAAACAAGATATGTGGGGGAAAATACAAAACTATGAGAAATTATTTGTGTGTG 27000

Qy      27001 CAGCACTGCTGAAAAAGATGATGGACAGGAGGAAGAAAATCGACGAGAGGTTTTGAAGGT 27060
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Db      27001 CAGCACTGCTGAAAAAGATGATGGACAGGAGGAAGAAAATCGACGAGAGGTTTTGAAGGT 27060

Qy      27061 CAATGGGGAAGTGAAGTTTTGTGTGTGGGGACCATGGAAATTTATTCAGGGGGCAAATTT 27120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      27061 CAATGGGGAAGTGAAGTTTTGTGTGTGGGGACCATGGAAATTTATTCAGGGGGCAAATTT 27120

Qy      27121 ACTTGTTGGTAGCCGAACGAACAACTTGACCGCGCATGCGAACCAATGAGTTCTCGGCAA 27180
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Db      27121 ACTTGTTGGTAGCCGAACGAACAACTTGACCGCGCATGCGAACCAATGAGTTCTCGGCAA 27180

Qy      27181 CCTCGGCACGCTCTTCGGCATTCTCGAGAGCGAGTTGGATCTGTCGGAATTTGGACAGAT 27240
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Db      27181 CCTCGGCACGCTCTTCGGCATTCTCGAGAGCGAGTTGGATCTGTCGGAATTTGGACAGAT 27240

Qy      27241 TCTGGGTGGCGACCTCTTCCTGAAAATTCAAACTTTTAGTTTTTGTAAATAAATTTGAAA 27300
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Db      27241 TCTGGGTGGCGACCTCTTCCTGAAAATTCAAACTTTTAGTTTTTGTAAATAAATTTGAAA 27300

Qy      27301 AAAAAAACAACATTTCACGACTCCAACTTTGTGGAATCATATTTGGTATTGCAAATTCAT 27360
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Qy      27361 GAAAACGTGAAACATAACTTTAAAGGCACACGCAGTTTTTAAAAGTTGGTCTCGCCACGA 27420
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Db      27361 GAAAACGTGAAACATAACTTTAAAGGCACACGCAGTTTTTAAAAGTTGGTCTCGCCACGA 27420

Qy      27421 CCTCTTATATTCAGTGCACTACTATGATCAAATAGTTGTACCTATACAATATAAGTCAAA 27480
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Qy      27481 TAATGGTCATTAGATCGAACAAAAGTTTAAGGATCGTAATCAAATATGATTTCAATTGGA 27540
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Qy      27541 AATTCCAATTTGAACTAAATAGGTACTATTGAATAAACTCTTTGAAATGTTGAAAAACAG 27600
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Qy      27601 GAATGATTACATCGGATCAATAAGTTTCAAATAATTATGTTAAACATTCCATTCGCTGAT 27660
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Qy      27661 AATTCGCTAATATTCGTTGAGGTTTTAGTTATTAATAAAGTATACATACCGCCTCTTCGA 27720
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Db      27661 AATTCGCTAATATTCGTTGAGGTTTTAGTTATTAATAAAGTATACATACCGCCTCTTCGA 27720

Qy      27721 TTTGTCTCTTTTGGACGCGAATCTTCTGTTGGAGCTTCTCGACGTTCTCTTGAAGTCTAT 27780
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Qy      27781 CGAACGCCTTCTTGTCTTCCTCGACTTGGAATTGAAGCTCACGAGCGCGTCTCTCCTGCT 27840
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Qy      27901 GGCTACGAACACGATCCTCGACCTTGGCCAATGCTTTGGCACCGACTGAAATATACAATT 27960
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Db      27901 GGCTACGAACACGATCCTCGACCTTGGCCAATGCTTTGGCACCGACTGAAATATACAATT 27960

Qy      27961 TTTCGACTTTAGAATACTTTGTTTGGTAACATACATTGGATCATGGCACGTTCAGCATCA 28020
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Qy      28021 TCGATCTTAGCCTGAAGTTCCTTGGCGTTGAGCTCGAGGGATTTGCGTTGTCTGTCGACA 28080
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Qy      28081 TGGACTGCATGCTCTTGTTCTTGACGGACCTCTTCAGCAAGACGATCCGCATCAGCAGCT 28140
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Db      28081 TGGACTGCATGCTCTTGTTCTTGACGGACCTCTTCAGCAAGACGATCCGCATCAGCAGCT 28140

Qy      28141 GCCTTGCGGGCACGCTCCTCTGAAGCCTTAAGCTCGTTCAAGTACTCGTCCAATTCGTTC 28200
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Qy      28201 TGAAAGTTTTATTTTTTAAAATCTGACAATCCGTTTAATAAACTCACTCTGGCAATCTGA 28260
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Qy      28261 ACCTCGTTCTCAACCTTTCTCTTCATGGCAGAAAGAGCAGCATTGTTTCCAATAAGCTCA 28320
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Db      28261 ACCTCGTTCTCAACCTTTCTCTTCATGGCAGAAAGAGCAGCATTGTTTCCAATAAGCTCA 28320

Qy      28321 GTGTTGGAAGACTTGAGTTCAGCCTGTTCGATTTCGAGTTGTTTCTTATGCTTATCAGAT 28380
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Db      28321 GTGTTGGAAGACTTGAGTTCAGCCTGTTCGATTTCGAGTTGTTTCTTATGCTTATCAGAT 28380

Qy      28381 GCCTCGATGCGGTGAGCAAGATCCTCGCTTTCAGAAAGAGCAATAGCAAGTCTCTTCTCA 28440
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Db      28381 GCCTCGATGCGGTGAGCAAGATCCTCGCTTTCAGAAAGAGCAATAGCAAGTCTCTTCTCA 28440

Qy      28441 GCAGCCAAATAGTTCTCACGGATCTCCTCACGTCTGCGTTGCTCATCATCGACTTGTCCT 28500
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Qy      28501 TGAAGTTCCTTGACTTGGTCGAAAAGTTTCTTCAAGTTCTTCTGGGCGTCAACGTTAGCC 28560
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Qy      28561 TTGTTGGCATGATCCAAAGCAATCTCGAGTTGATTGATGTCAGTCTCAAGCTTCTTCTTG 28620
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Db      28561 TTGTTGGCATGATCCAAAGCAATCTCGAGTTGATTGATGTCAGTCTCAAGCTTCTTCTTG 28620

Qy      28621 GCTCTGGCGAGCTCGGCCTTGCTCTTAGCTTCGGTTTCGAGGGAAGCTTGGATGGACTCG 28680
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Db      28621 GCTCTGGCGAGCTCGGCCTTGCTCTTAGCTTCGGTTTCGAGGGAAGCTTGGATGGACTCG 28680

Qy      28681 AGGGCACGTTGATGGTTCTTGCGAGTGTTCTCGAATTCCTCCTCCTTCTCTTGAATTCTC 28740
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Qy      28741 TTCTCGATTTCTGAACGGATCTGTTGAACCTCGATTTGAAGACGGAGAACCTTGCTCTCT 28800
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Qy      28801 TCGGCTTCAAGTGCAGCCTCGGCCTCATCAAGAGCATGTTGAAGCTCGTCCTTTTCTTGT 28860
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Qy      28861 TCGAGACGGCGGACAGACTTGTGAACCTCTTGGTATGTACGTCCTCCTTGGGTGATTTGC 28920
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Qy      28921 TCGTTAATGTCGCGAATCTCTTGCGAAAAGATCTTGTTCTCGCGTCTCAAGGTCTCGATT 28980
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Qy      28981 TGCTCGCTGAGGTTGTCCATGGATGAACGAAGTTTGAAGACTTCAGTCGAGGTATTACGG 29040
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Db      28981 TGCTCGCTGAGGTTGTCCATGGATGAACGAAGTTTGAAGACTTCAGTCGAGGTATTACGG 29040

Qy      29041 CTGTCACGAGTAGTGGCATCAATCTCTTTTTGGATATCATCAACCTTTCTCTTCCAGTCA 29100
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Qy      29101 TCAACGATCTTGTCGAAAGCACGTTGTTTCTTTTCAAGGGAAGCAATGACAGTCAAGTGA 29160
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Qy      29161 CGATCAACATCTGAACGAGCATCTTCGGTTTCGGCAAGAAGTTTTCCCTTGGCCTTCTCG 29220
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Qy      29341 CTGGCCTTCCATTGAGAAATCTCGGAATTGATACGGGAAAGTTGACGTTGAATGTCGTCT 29400
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Qy      29521 TCTACAAGTTGAGAAGAGAATGCAGTCTTGGCACGGTTGATGGTAGCCAAATGAATCTCG 29580
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Db      29821 TTAGACTTCTGAAGAGCATCCAAGGTGTTGGTCAAGGCAGAAATTTGGTCATTGTTCTTT 29880

Qy      29881 CTGCGTATCATAGCCATCTGATCTTCGTTGGCCATGTTCTTCTCGTCAAGATCTCTGCGG 29940
Db      29881 CTGCGTATCATAGCCATCTGATCTTCGTTGGCCATGTTCTTCTCGTCAAGATCTCTGCGG 29940

Qy      29941 AACTTGATGATTTCAGAATCCTTCTTCTTGTTGTTGTCTTGTTGGATTTCGAGTTGCTTG 30000
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Qy      30001 TTCTGTTCGTCAAGTCTCTCGTTGAGCTCATCAAGCTCGCGTTGAAGCTCAGCACGAGCA 30060
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Qy      30121 CGTTGAGCATTTTCCTTGGATTGGCGGGTAAGTCTGTTGGCAAGTGCTTGCTCATCCTCA 30180
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Db      30301 TTTCTCTTAGATTTCTCAGTTTCAGCTCTGATTCTCTTCTCTCTTTCAACAGCTTCTTCC 30360

Qy      30361 ATTTCGTCCAAAGTTTGCTCGAGCTTTCCACGAAGTCGGTTGGCTTGAGCTTGCTTGGCT 30420
Db      30361 ATTTCGTCCAAAGTTTGCTCGAGCTTTCCACGAAGTCGGTTGGCTTGAGCTTGCTTGGCT 30420

Qy      30421 TCTTCAGCTTGAAGATCGTCGACAAGTTGACGGTTGTTCTCTTCAAGAAGCTTCTTCTCC 30480
Db      30421 TCTTCAGCTTGAAGATCGTCGACAAGTTGACGGTTGTTCTCTTCAAGAAGCTTCTTCTCC 30480

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Db      30541 TGGTTTTCCTTGGCGGCCTTCTCCTCAAGAGATTTAGCCAAGTTTCCATCTACGGCTTCG 30600

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Db      30661 GCGTTCTTCTCTTCATGCTCCGAAAGACGGTCGTTGGCGTCATTCAGAGACTTCTCAACT 30720

Qy      30721 TCTTGACGAGCACTGTTGAGGCGGGTAAGCTTCTCTTCGATGGCAGCAGATCCTCCTTGG 30780
Db      30721 TCTTGACGAGCACTGTTGAGGCGGGTAAGCTTCTCTTCGATGGCAGCAGATCCTCCTTGG 30780

Qy      30781 GTAAGCTCGAGAGCTTCCAAAAGTTTTGATCTCTCAGCGGACAGCTTGGCGTAAGCCTCT 30840
Db      30781 GTAAGCTCGAGAGCTTCCAAAAGTTTTGATCTCTCAGCGGACAGCTTGGCGTAAGCCTCT 30840

Qy      30841 TCTTGAGATTTTCTGGCAGATTCGGCCTTCTTGGCTTCAGCTTCAAGAACCTTTTGCTCT 30900
Db      30841 TCTTGAGATTTTCTGGCAGATTCGGCCTTCTTGGCTTCAGCTTCAAGAACCTTTTGCTCT 30900

Qy      30901 TCAGCCATCTT 30911
Db      30901 TCAGCCATCTT 30911
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Search completed: October 22, 2003, 15:12:01
Job time : 1141 secs

GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: October 23, 2003, 06:28:11 ; Search time 14 Seconds
(without alignments)
2.199 Million cell updates/sec

Title: us-09-872-523-5
Perfect score: 2656
Sequence: 1 MSEFLKIVRANKKSDRKLDK.....PIGWCEAHSYVLQPPKKYNY 498

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1 seqs, 30911 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=soft -Q=us-09-872-523-5 -DB=23-jul-1999-z71266
-SUFFIX=pto -OUT=align5_old -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits
-START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=1 -DOCALIGN=200
-THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=1 -MODE=LOCAL -OUTFMT=pto
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -NCPU=6 -NO_XLPXY
-NEG_SCORES=0 -LONGLOG -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : 23-jul-1999-z71266:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	2520.5	94.9	30911	1	CER06C7	ACCESSION:Z71266

ALIGNMENTS

RESULT 1
CER06C7/c
LOCUS CER06C7 30911 bp DNA linear INV 23-JUL-1999
DEFINITION Caenorhabditis elegans cosmid R06C7, complete sequence.
ACCESSION Z71266
VERSION Z71266.1 GI:1279324
KEYWORDS HTG; Adenylosuccinate lyase; Myosin heavy chain; Rat TOAD-64 protein like; Serine/threonine-protein kinase; Zinc finger protein.
SOURCE Caenorhabditis elegans
ORGANISM Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE 1 (bases 1 to 30911)
AUTHORS Wilson,R., Ainscough,R., Anderson,K., Baynes,C., Berks,M., Bonfield,J., Burton,J., Connell,M., Copsey,T., Cooper,J., Coulson,A., Craxton,M., Dear,S., Du,Z., Durbin,R., Favello,A., Fulton,L., Gardner,A., Green,P., Hawkins,T., Hillier,L., Jier,M., Johnston,L., Jones,M., Kershaw,J., Kirsten,J., Laister,N., Latreille,P., Lightning,J., Lloyd,C., McMurray,A., Mortimore,B., O'Callaghan,M., Parsons,J., Percy,C., Rifken,L., Roopra,A., Saunders,D., Shownkeen,R., Smaldon,N., Smith,A., Sonnhammer,E., Staden,R., Sulston,J., Thierry-Mieg,J., Thomas,K., Vaudin,M., Vaughan,K., Waterston,R., Watson,A., Weinstock,L., Wilkinson-Sproat,J. and Wohldman,P.
TITLE 2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans
JOURNAL Nature 368 (6466), 32-38 (1994)
MEDLINE 94150718
REFERENCE 2 (bases 1 to 30911)
AUTHORS Gardner,A.
TITLE Direct Submission
JOURNAL Submitted (19-APR-1996) Louis, MO 63110, USA. E-mail: jes@sanger.ac.uk or rw@nematode.wustl.edu
COMMENT Coding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Washington), and other available information.
For a graphical representation of this sequence and its analysis see:-
http://webace.sanger.ac.uk/cgi-bin/display?db=wormace&class=Sequence &object=R06C7
Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.
IMPORTANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.
IMPORTANT: This sequence is not the entire insert of clone R06C7. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.
The true left end of clone R06C7 is at 1 in this sequence. The true right end of clone R06C7 is at 8718 in sequence Z71261.
The true left end of clone F21C3 is at 30808 in this sequence. The start of this sequence (1..106) overlaps with the end of sequence Z98261.
The end of this sequence (30808..30911) overlaps with the start of sequence Z71261.
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Best Local Similarity:  80.75%          Mismatches:     1
Query Match:            94.90%          Indels:         116
DB:                     1               Gaps:           5

us-09-872-523-5 (1-498) x CER06C7 (1-30911)

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Qy        116 ------------------------------------------------------------ 116

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Job time : 21 secs

$\frac{426}{155}$ / 271 aa

at least

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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: October 23, 2003, 06:22:06 ; Search time 23 Seconds
(without alignments)
4.024 Million cell updates/sec

Title: us-09-872-523-6
Perfect score: 1497
Sequence: 1 atgtctgaatttctgaaaat.....cgaaaaagtacaactattga 1497

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 30911 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1 summaries

Database : 23-jul-1999-z71266:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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ALIGNMENTS

RESULT 1
CER06C7/c
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DEFINITION Caenorhabditis elegans cosmid R06C7, complete sequence.
ACCESSION Z71266
VERSION Z71266.1 GI:1279324
KEYWORDS HTG; Adenylosuccinate lyase; Myosin heavy chain; Rat TOAD-64 protein like; Serine/threonine-protein kinase; Zinc finger protein.
SOURCE Caenorhabditis elegans
ORGANISM Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE 1 (bases 1 to 30911)
AUTHORS Wilson,R., Ainscough,R., Anderson,K., Baynes,C., Berks,M., Bonfield,J., Burton,J., Connell,M., Copsey,T., Cooper,J., Coulson,A., Craxton,M., Dear,S., Du,Z., Durbin,R., Favello,A., Fulton,L., Gardner,A., Green,P., Hawkins,T., Hillier,L., Jier,M., Johnston,L., Jones,M., Kershaw,J., Kirsten,J., Laister,N., Latreille,P., Lightning,J., Lloyd,C., McMurray,A., Mortimore,B., O'Callaghan,M., Parsons,J., Percy,C., Rifken,L., Roopra,A., Saunders,D., Shownkeen,R., Smaldon,N., Smith,A., Sonnhammer,E., Staden,R., Sulston,J., Thierry-Mieg,J., Thomas,K., Vaudin,M., Vaughan,K., Waterston,R., Watson,A., Weinstock,L., Wilkinson-Sproat,J. and Wohldman,P.
TITLE 2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans
JOURNAL Nature 368 (6466), 32-38 (1994)
MEDLINE 94150718
REFERENCE 2 (bases 1 to 30911)
AUTHORS Gardner,A.
TITLE Direct Submission
JOURNAL Submitted (19-APR-1996) Louis, MO 63110, USA. E-mail: jes@sanger.ac.uk or rw@nematode.wustl.edu
COMMENT Coding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Washington), and other available information.
For a graphical representation of this sequence and its analysis see:-
http://webace.sanger.ac.uk/cgi-bin/display?db=wormace&class=Sequence &object=R06C7
Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.
IMPORTANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.
IMPORTANT: This sequence is not the entire insert of clone R06C7. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.
The true left end of clone R06C7 is at 1 in this sequence. The true right end of clone R06C7 is at 8718 in sequence Z71261.
The true left end of clone F21C3 is at 30808 in this sequence. The start of this sequence (1..106) overlaps with the end of sequence Z98261.
The end of this sequence (30808..30911) overlaps with the start of sequence Z71261.
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complement(Z71258.1:39857..39994),
complement(Z71258.1:39258..39701),
complement(Z71258.1:38262..39212),
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Qy       1277 G---------------------------------------------------------- 1277
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